prejudice or disclaimer; amended claims 15 and 19; and added new claims 35-84. Accordingly, upon entry of this Amendment, claims 15-22 as amended and new claims 35-84 will be pending; and claims 15-17, 19-21, and 35-84 will be under examination.

Applicants maintain that the amendments to the specification and to claims 15 and 19, and the addition of new claims 35-84 do not raise an issue of new matter.

Applicants have amended the specification to conform to the corrected drawings filed on September 3, 2002.

Support for the amendments to claims 15 and 19 and new claims 35-84 can be found in the previous version of claims 15-17 and 19-21 and in the specification *inter alia* at least on page 4, lines 5-8; page 14, lines 9-19; page 15, line 10 through page 19, line 9; page 20, line 13 through page 21, line 6; page 29, lines 1-5 and 25-27; Figure 1 and 1A-1 to 1A-107; and Figure 2 and 2A-1 to 2A-19.

Accordingly, applicants respectfully request that the Amendments be entered.

Withdrawal of Claims 18 and 22 from Consideration by the Examiner

On page 2 of the December 3, 2002 Office Action, the Examiner withdrew dependent claims 18 and 22 from consideration because these claims are drawn to an activator of ACPS. Applicants maintain that independent claims 15 and 19, from which claims 18 and 22 depend, are "linking claims." Pursuant to MPEP §809.04, applicants request that the Examiner examine claims 18 and 22 on their merits if linking claims 15 and 19 are determined to be allowable.

Objections to the Specification

On page 2 of the Office Action, the Examiner stated that the corrected drawings filed on September 3, 2002 have been accepted and necessitate corrections to be made to the Specification.

Applicants have hereinabove amended the Specification to conform to the corrected drawings. Accordingly, applicants respectfully request that the Examiner withdraw this objection.

Rejections under 35 U.S.C. §112, first paragraph

On page 3 of the December 3, 2002 Office Action, the Examiner rejected claims 15-17 and 19-21 under 35 U.S.C. §112, first paragraph, for containing subject matter which allegedly is not described in the specification in such a way as to enable one skilled in the art to make and/or use the invention. The Examiner acknowledged that the specification is enabling for a crystal structure of ACPS and ACPS-CoA complex (Example 1, pages 22-36) which have atom coordinates instantly disclosed (Figures 1-2A-19).

Applicants believe that the bases for this rejection should be moot in view of the amendments to claims 15 and 19 and the addition of new claims 35-84. The independent claims now recite characteristics of crystallized ACPS or the crystallized ACPS-CoA complex. Applicants maintain that the subject application provides a disclosure that enables one skilled in the art to make and use the claimed invention. Accordingly, applicants respectfully request that the Examiner withdraw this ground of rejection.

Rejections under 35 U.S.C. §112, second paragraph

On page 4 of the December 3, 2002 Office Action, the Examiner rejected claims 15-17 and 19-21 under 35 U.S.C. §112, second paragraph, as being indefinite for reciting the abbreviation ACPS.

Applicants have amended independent claim 15 to recite "acyl carrier protein synthase (ACPS)" and have amended independent claim 19 to recite "acyl carrier protein

synthase-coenzyme A (ACPS-CoA) complex". Accordingly, applicants respectfully request that the Examiner withdraw this ground of rejection.

Rejections under 35 U.S.C. §103(a)

On page 5 of the December 3, 2002 Office Action, the Examiner rejected claims 15-17 and 19-21 under 35 U.S.C. §103(a) as being unpatentable over Rosowsky et al. (1999) in view of *In re Gulack*, 703 F.2d 1381, 1385, 217 USPQ 401, 404 (Fed. Cir. 1983) taken with Ahern (The Scientist, 1996). The Examiner stated that Rosowsky et al. (1999) disclose a method for designing based on the 3D structure of enzyme-inhibitor complexes by X-ray crystallography. The Examiner acknowledged that the method disclosed by Rosowsky et al. does not specify that the active sites were identified by crystal structure coordinates and the three-dimensional model of Acyl Carrier Protein Synthetase (ACPS); however, the Examiner stated that the specific limitations of crystal structure coordinates and the three-dimensional model of ACPS in this instant case do not distinguish the invention from the prior art in term of patentability because they are descriptive nonfunctional subject matter. The Examiner stated that *In re Gulack* defines nonfunctional descriptive material, as when descriptive material is not functionally related to the substrate, the descriptive material will not distinguish the invention from the prior art in term of patentability. The Examiner cited Ahern (1996) as evidence of the current state of art for computational modeling. The Examiner concluded that it would have been obvious to one having ordinary skill in the art at the time of the invention was made to use the commercially available software, Sybyl, taught by Ahern and the investigation type of method taught by Rosowsky et al. to model the crystal structure of ACPS and identify agents that interact with it.

On page 7 of the December 3, 2002 Office Action, the Examiner rejected claims 15-17 under 35 U.S.C. §103(a) as being unpatentable over Rosowsky et al. (1999), taken in view with Ahern (The Scientist, 1996) taken in view of Qiu et al. (1999). The

Examiner's comments with regard to Rosowsky et al. and Ahern are the same as summarized above. The Examiner stated that Qiu et al. disclose the crystal structure for β-Ketoacyl-acyl carrier synthase III (FabH) and that the crystal structures of FabH were determined in the presence and absence of acetyl-CoA. The Examiner concluded that it would have been obvious to one having ordinary skill in the art at the time the invention was made to use the commercially available software, Sybyl, taught by Ahern and the investigation type of method taught by Rosowsky et al. with the β-Ketoacyl-acyl carrier synthase III (FabH) disclosed by Qiu et al. to identify agents that interact with ACPS based on 3D coordinate data.

Applicants have hereinabove amended claims 15 and 19 and added new independent claims 35, 68, 71, and 74, wherein step (a) of each independent claim recites the step of obtaining either a crystallized ACPS or a crystallized ACPS-CoA complex that is characterized by features which applicants maintain are novel and nonobvious. Since the Examiner is adopting the position that no patentable weight is given to the structural coordinates in the claimed method, a position with which applicants respectfully do not concur, applicants have added new claims 68-84, which are analogous to claims 15-17, 19-21, and 35-45, with the exception that claims 68-84 do not recite the structural coordinates.

Applicants maintain that the references cited by the Examiner do not teach or suggest every element of the claimed invention. In particular, applicants maintain that cited references do not teach or suggest *inter alia* step (a) of independent claims 15, 19, 35, 68, 71, and 74. Accordingly, applicants maintain that the claims as a whole are not rendered obvious by the cited references.

As further evidence of the nonobviousness of the subject invention, applicants note the Examiner's comment on page 4, lines 1-3 of the Office Action: "It is well documented that protein crystallization is in essence a trial-and-error method, and the results are unpredictable (Drenth, J.)."

Applicants respectfully request that the Examiner reconsider and withdraw this ground of rejection.

CONCLUSIONS

In view of the amendments and remarks made hereinabove, applicants respectfully request that the Examiner reconsider and withdraw the objections and rejections set forth in the December 3, 2002 Office Action and earnestly solicit allowance of the claims now under examination, i.e. claims 15-17, 19-21, and 35-84.

A check for $432.00 is enclosed to cover the fee for filing claims in addition to the maximum number previously paid for (24 claims in excess of 34 claims previously paid for, 24 claims x $18.00/excess claim = $432.00). No additional fee is deemed necessary in connection with the filing of this Amendment. However, if any other fee is required to preserve the pendency of the subject application, authorization is hereby given to charge the amount of any such fee to Deposit Account No. 01-1785.

Respectfully submitted,

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Dated: March 3, 2003
New York, New York

By _____
Craig J. Arnold, Reg. No. 34,287
Alan D. Miller, Reg. No. 42,889

Marked-up Amendments to the Specification

Additions are underlined. There are no deletions.

On page 5, lines 8-25:

--Yet another aspect of the present invention is a method for identifying an activator or inhibitor of any molecule or molecular complex which comprises a CoA binding site, including any member of the ACPS-like P-pant transferases, comprising the steps of generating a three dimensional model of said molecule or molecular complex using the relative structural coordinates according to Figure 1 and 1A-1 to 1A-107 or Figure 2 and 2A-1 to 2A-19 of residues ARG45, PHE49, ARG53, LYS81, ASN84, GLY85, LYS86, PRO87, ILE103, THR104 and HIS105 from one monomer of ACPS, and of ASP8, GLU11, ARG14, MET18, PHE25, ARG28, ILE29, PHE54, GLU58, SER61, LYS62, GLY65, THR66, GLY67, ILE68 and PHE74 from a second monomer of ACPS, ± a root mean square deviation from the backbone atoms of said residues of not more than 1.5Å, and then selecting or designing a candidate activator or inhibitor that interacts with said molecule or molecular complex using computer fitting analyses of interactions between the three dimensional model of the molecule or molecular complex and the candidate activator or inhibitor. The effect of the candidate activator or inhibitor may be evaluated by obtaining the candidate activator or inhibitor, contacting the same with the molecule or molecular complex, and measuring the effect of the candidate activator or inhibitor on molecular or molecular complex activity.--

On page 5, line 26 through page 6, line 11:

--Alternatively, the three dimensional model of the molecule or molecular complex comprising a CoA binding site may be determined using the relative structural coordinates according to Figure 1 and 1A-1 to 1A-107 or Figure 2 and 2A-1 to 2A-19 of residues ARG53, ASN84, GLY85, LYS86, PRO87, ILE103, THR104, and HIS105 from one monomer of ACPS and ASP8, PHE25, ARG28, ILE29, PHE54, GLU58, SER61, LYS62, GLY65, THR66, GLY67, ILE68 and PHE74 from a second monomer of ACPS, or alternatively, of residues LEU41, ARG45, GLU48, PHE49, LEU50, ALA51, GLY52, ILE79,

ARG80, LYS81, ASP82, GLN83, TYR88, VAL101, SER102, THR106, TYR109, ALA110, and ALA111 from one monomer of ACPS and ILE5, GLY6, LEU7, ILE9, THR10, ARG14, ILE15, MET18, GLN22, ALA55, LYS57, ALA59, PHE60, ALA63, PHE64, GLY69, ARG70, GLN71 and LEU72 from a second monomer of ACPS, in each case ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å. Also provided by the present invention are the activators or inhibitors selected or designed using the above-noted methods.--

On page 6, line 22 through page 7, line 14:

--Finally, the present invention provides the CoA active site of an ACPS-like P-pant transferase, including, but not limited to, an ACPS, comprising, alternatively, (a) the relative structural coordinates according to Figure 1 and 1A-1 to 1A-107 of ARG45, PHE49, ARG53, LYS81, ASN84, GLY85, LYS86, PRO87, ILE103, THR104 and HIS105 from one monomer of ACPS, and ASP8, GLU11, ARG14, MET18, PHE25, ARG28, ILE29, PHE54, GLU58, SER61, LYS62, GLY65, THR66, GLY67, ILE68 and PHE74 from a second monomer of ACPS, in each case ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å, (b) the structural coordinates according to Figure 1 and 1A-1 to 1A-107 of residues ARG53, ASN84, GLY85, LYS86, PRO87, ILE103, THR104, and HIS105 from one monomer of ACPS and ASP8, PHE25, ARG28, ILE29, PHE54, GLU58, SER61, LYS62, GLY65, THR66, GLY67, ILE68 and PHE74 from a second monomer of ACPS, in each case ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å, or (c) the structural coordinates according to Figure 1 and 1A-1 to 1A-107 of residues LEU41, ARG45, GLU48, PHE49, LEU50, ALA51, GLY52, ILE79, ARG80, LYS81, ASP82, GLN83, TYR88, VAL101, SER102, THR106, TYR109, ALA110, and ALA111 from one monomer of ACPS and ILE5, GLY6, LEU7, ILE9, THR10, ARG14, ILE15, MET18, GLN22, ALA55, LYS57, ALA59, PHE60, ALA63, PHE64, GLY69, ARG70, GLN71 and LEU72 from a second monomer of ACPS, in each case ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å.--

On page 7, line 15 through page 8, line 8:

--In an additional embodiment, the present invention provides the CoA active site of an ACPS-like P-pant transferase, including, but not limited to, an ACPS, wherein said active site is in its bound configuration, and comprising alternatively, (a) the relative structural coordinates according to Figure 2 and 2A-1 to 2A-19 of ARG45, PHE49, ARG53, LYS81, ASN84, GLY85, LYS86, PRO87, ILE103, THR104 and HIS105 from one monomer of ACPS, and ASP8, GLU11, ARG14, MET18, PHE25, ARG28, ILE29, PHE54, GLU58, SER61, LYS62, GLY65, THR66, GLY67, ILE68 and PHE74 from a second monomer of ACPS, in each case ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å, (b) the structural coordinates according to Figure 2 and 2A-1 to 2A-19 of residues ARG53, ASN84, GLY85, LYS86, PRO87, ILE103, THR104, and HIS105 from one monomer of ACPS and ASP8, PHE25, ARG28, ILE29, PHE54, GLU58, SER61, LYS62, GLY65, THR66, GLY67, ILE68 and PHE74 from a second monomer of ACPS, in each case ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å, or (c) the structural coordinates according to Figure 2 and 2A-1 to 2A-19 of residues LEU41, ARG45, GLU48, PHE49, LEU50, ALA51, GLY52, ILE79, ARG80, LYS81, ASP82, GLN83, TYR88, VAL101, SER102, THR106, TYR109, ALA110, and ALA111 from one monomer of ACPS and ILE5, GLY6, LEU7, ILE9, THR10, ARG14, ILE15, MET18, GLN22, ALA55, LYS57, ALA59, PHE60, ALA63, PHE64, GLY69, ARG70, GLN71 and LEU72 from a second monomer of ACPS, in each case ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å.--

On page 8, lines 11-19:

--Figure 1 and 1A-1 to 1A-107 lists the atomic structure coordinates for ACPS as derived by X-ray diffraction of an ACPS crystal. "Atom type" refers to the atom whose coordinates are being measured. "Residue" refers to the type of residue of which each measured atom is a part - i.e., amino acid, cofactor, ligand or solvent. The "x, y and z" coordinates indicate the Cartesian coordinates of each measured atom's location in the unit cell (Å). "Occ" indicates the occupancy factor. "B" indicates the "B-value", which is

a measure of how mobile the atom is in the atomic structure (Å^2). "MOL" indicates the segment identification used to uniquely identify each molecule.--

On page 8, lines 20-22:

--Figure 2 and 2A-1 to 2A-19 lists the atomic structure coordinates for ACPS and CoA as derived by X-ray diffraction of an ACPS-CoA crystal. Figure headings are as noted above.--

On page 10, line 23 through page 11, line 10:

--As used herein, the protein used in the ACPS crystals and crystal complexes of the present invention includes any protein (i.e., as used herein, any protein, polypeptide or peptide), isolated from any source (including, but not limited to, a protein isolated from *Aquifex*, *Chlamydophila*, *Helicobacter*, *Staphylococcus*, *Thermotoga*, *Escherichia*, *Rickettsia*, *Streptomyces*, *Treponema*, *Bacillus*, *Bradyrhizobium*, and *Mycobacterium*), wherein said protein has ACPS-like P-pant transferase activity, and further comprises the consensus sequence as shown in Figure 9. Additionally, the protein used in the ACPS crystals and crystal complexes of the present invention includes proteins having ACPS-like P-pant transferase activity which comprise the relative structural coordinates according to Figure 1 and 1A-1 to 1A-107 or Figure 2 and 2A-1 to 2A-19 for the residues GLY6, ASP8, ALA51, LYS57, GLU58, ARG53, ALA59, LYS62 and ALA63, ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å, or more preferably not more than 1.0Å, or most preferably, not more than 0.5Å. In a preferred embodiment of the invention and as exemplified below, ACPS is cloned and isolated from *B. subtilis*, and then overexpressed in a commercially available *E. coli* system.--

On page 11, lines 11-25:

--In an alternate embodiment of the present invention, the ACPS used to generate the crystals and/or crystal complexes of the present invention comprises amino acid residues ASP8, GLU11, ARG14, MET18, PHE25, ARG28, ILE29, ARG45, PHE49,

ARG53, PHE54, GLU58, SER61, LYS62, GLY65, THR66, GLY67, ILE68, PHE74, LYS81, ASN84, GLY85, LYS86, PRO87, ILE103, THR104, and HIS105, or conservative substitutions thereof. These amino acids constitute a depression which defines the CoA active site in the three dimensional structure of the ACPS enzyme, wherein the depression is more particularly comprised of the relative structural coordinates according to Figure 1 and 1A-1 to 1A-107 or Figure 2 and 2A-1 to 2A-19 of residues ARG45, PHE49, ARG53, LYS81, ASN84, GLY85, LYS86, PRO87, ILE103, THR104 and HIS105 from one monomer of ACPS, and residues ASP8, GLU11, ARG14, MET18, PHE25, ARG28, ILE29, PHE54, GLU58, SER61, LYS62, GLY65, THR66, GLY67, ILE68 and PHE74 from a second molecule of ACPS, ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å, or more preferably not more than 1.0Å, or most preferably, not more than 0.5Å.--

On page 11, line 26 through page 12, line 8:

--There are six ACPS molecules in the asymmetric unit of the ACPS crystal. In one embodiment of the invention, the relative structural coordinates according to Figure 1 and 1A-1 to 1A-107 of the two monomers forming the depression defining the CoA active site are of residues ARG45, PHE49, ARG53, LYS81, ASN84, GLY85, LYS86, PRO87, ILE103, THR104 and HIS105 from ACPS1, and residues ASP8, GLU11, ARG14, MET18, PHE25, ARG28, ILE29, PHE54, GLU58, SER61, LYS62, GLY65, THR66, GLY67, ILE68 and PHE74 from ACPS2. In alternate embodiments, the relative structural coordinates according to Figure 1 and 1A-1 to 1A-107 are from ACPS2 and ACPS3, respectively; from ACPS1 and ACPS3, respectively; from ACPS4 and ACPS5, respectively; from ACPS5 and ACPS6, respectively; and from ACPS4 and ACPS6, respectively.--

On page 12, lines 9-26:

--In an alternate preferred embodiment, the ACPS used to generate the crystals and/or crystal complexes of the present invention comprises amino acid residues which are within 4Å of the CoA molecule associated with the ACPS CoA binding site. In a specific embodiment, the ACPS comprises amino acid residues ASP8, PHE25, ARG28,

ILE29, ARG53, PHE54, GLU58, SER61, LYS62, GLY65, THR66, GLY67, ILE68, PHE74, ASN84, GLY85, LYS86, PRO87, ILE103, THR104, and HIS105, or conservative substitutions thereof. Such residues specifically comprise the relative structural coordinates according to Figure 1 and 1A-1 to 1A-107 or Figure 2 and 2A-1 to 2A-19 of residues ARG53, ASN84, GLY85, LYS86, PRO87, ILE103, THR104, and HIS105 from one monomer of ACPS and ASP8, PHE25, ARG28, ILE29, PHE24, GLU58, SER61, LYS62, GLY65, THR66, GLY67, ILE68, and PHE74 from a second monomer of ACPS, ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å, or more preferably not more than 1.0Å, or most preferably, not more than 0.5Å. In alternate embodiments, the relative structural coordinates according to Figure 1 and 1A-1 to 1A-107 are from ACPS1 and ACPS2, respectively; from ACPS2 and ACPS3, respectively; from ACPS1 and ACPS3, respectively; from ACPS4 and ACPS5, respectively; from ACPS5 and ACPS6, respectively; and from ACPS4 and ACPS6, respectively.--

On page 12, line 27 through page 13, line 20:

--In yet another alternate preferred embodiment, the ACPS used to generate the crystals and/or crystal complexes of the present invention comprises amino acid residues which are within 4Å to 8Å of the CoA molecule associated with the ACPS CoA binding site. Specifically, such residues include ILE5, GLY6, LEU7, ILE9, THR10, ARG14, ILE15, MET18, GLN22, LEU41, ARG45, GLU48, PHE49, LEU50, ALA51, GLY52, ALA55, LYS57, ALA59, PHE60, ALA63, PHE64, GLY69, ARG70, GLN71, LEU72, ILE79, ARG80, LYS81, ASP82, GLN83, TYR88, VAL101, SER102, THR106, TYR109, ALA110, and ALA111, or conservative substitutions thereof. Such residues more particularly comprise the relative structural coordinates according to Figure 1 and 1A-1 to 1A-107 or Figure 2 and 2A-1 to 2A-19 of residues LEU41, ARG45, GLU48, PHE49, LEU50, ALA51, GLY52, ILE79, ARG80, LYS81, ASP82, GLN83, TYR88, VAL101, SER102, THR106, TYR109, ALA110, and ALA111 from one monomer of ACPS and ILE5, GLY6, LEU7, ILE9, THR10, ARG14, ILE15, MET18, GLN22, ALA55, LYS57, ALA59, PHE60, ALA63, PHE64, GLY69, ARG70, GLN71 and LEU72 from a second monomer of ACPS, ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å (or more preferably

not more than 1.0Å, or most preferably, not more than 0.5Å), and more specifically may comprise the relative structural coordinates of residues according to Figure 1 and 1A-1 to 1A-107 from ACPS1 and ACPS2, respectively; from ACPS2 and ACPS3, respectively; from ACPS1 and ACPS3, respectively; from ACPS4 and ACPS5, respectively; from ACPS5 and ACPS6, respectively; and from ACPS4 and ACPS6, respectively.--

On page 13, lines 21-26:

--Further, the ACPS used to generate the crystals and/or crystal complexes of the present invention may comprise the entire 121 amino acid residues of Figure 8, and the structural coordinates of these residues according to Figure 1 and 1A-1 to 1A-107 or Figure 2 and 2A-1 to 2A-19, ± a root mean square deviation from the backbone atoms of said amino acid residues of not more than 1.5Å, or more preferably not more than 1.0Å, or most preferably, not more than 0.5Å.--

On page 15, lines 10-28:

--As used herein, an "active site" refers to a region of a molecule or molecular complex that, as a result of its shape and charge potential, interacts with another agent (including, without limitation, a protein, polypeptide, peptide, nucleic acid, including DNA or RNA, molecule, compound, antibiotic or drug). The agent may be an activator or inhibitor of the molecular or molecular complex activity. The present invention is directed to a CoA active site of an ACPS-like P-pant transferase, including the active site of an acyl carrier protein synthase, comprising the relative structural coordinates according to Figure 1 and 1A-1 to 1A-107 of residues ARG45, PHE49, ARG53, LYS81, ASN84, GLY85, LYS86, PRO87, ILE103, THR104 and HIS105 from one monomer of ACPS, and of ASP8, GLU11, ARG14, MET18, PHE25, ARG28, ILE29, PHE54, GLU58, SER61, LYS62, GLY65, THR66, GLY67, ILE68 and PHE74 from a second monomer of ACPS, in each case ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å, or more preferably not more than 1.0Å, or most preferably, not more than 0.5Å. More specifically, the active site of ACPS in its native (i.e., unbound) state may comprise the relative structural coordinates of the residues

according to Figure 1 and 1A-1 to 1A-107 from ACPS1 and ACPS2, respectively; from ACPS2 and ACPS3, respectively; from ACPS1 and ACPS3, respectively; from ACPS4 and ACPS5, respectively; from ACPS5 and ACPS6, respectively; and from ACPS4 and ACPS6, respectively.---

On page 16, lines 1-12:

--In an alternate embodiment, the CoA active site of the present invention comprises the relative structural coordinates according to Figure 1 and 1A-1 to 1A-107 of residues ARG53, ASN84, GLY85, LYS86, PRO87, ILE103, THR104, and HIS105 from one monomer of ACPS and of residues ASP8, PHE25, ARG28, ILE29, PHE54, GLU58, SER61, LYS62, GLY65, THR66, GLY67, ILE68 and PHE74 from a second monomer of ACPS, in each case ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å, or more preferably not more than 1.0Å, or most preferably, not more than 0.5Å. The active site may comprise the relative structural coordinates of the residues according to Figure 1 and 1A-1 to 1A-107 from ACPS1 and ACPS2, respectively; from ACPS2 and ACPS3, respectively; from ACPS1 and ACPS3, respectively; from ACPS4 and ACPS5, respectively; from ACPS5 and ACPS6, respectively; and from ACPS4 and ACPS6, respectively.---

On page 16, lines 13-26:

--In a yet further embodiment, the CoA active site of the present invention comprises the relative structural coordinates according to Figure 1 and 1A-1 to 1A-107 of residues LEU41, ARG45, GLU48, PHE49, LEU50, ALA51, GLY52, ILE79, ARG80, LYS81, ASP82, GLN83, TYR88, VAL101, SER102, THR106, TYR109, ALA110, and ALA111 from one monomer of ACPS and of residues ILE5, GLY6, LEU7, ILE9, THR10, ARG14, ILE15, MET18, GLN22, ALA55, LYS57, ALA59, PHE60, ALA63, PHE64, GLY69, ARG70, GLN71 and LEU72 from a second monomer of ACPS, in each case ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å, or more preferably, not more than 1.0Å, and most preferably, not more than 0.5Å. The active site may comprise the relative structural coordinates of the residues according to Figure

1 and 1A-1 to 1A-107 from ACPS1 and ACPS2, respectively; from ACPS2 and ACPS3, respectively; from ACPS1 and ACPS3, respectively; from ACPS4 and ACPS5, respectively; from ACPS5 and ACPS6, respectively; and from ACPS4 and ACPS6, respectively.--

On page 16, line 27 through page 17, line 4:

--Further still, an alternate embodiment of the CoA active site of the present invention comprises the relative structural coordinates according to Figure 1 and 1A-1 to 1A-107 of GLY6, ASP8, ALA51, ARG53, LYS57, GLU58, ALA59, LYS62 and ALA63, ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å, or more preferably, not more than 1.0Å, and most preferably, not more than 0.5Å.--

On page 17, lines 12-20:

--In a preferred embodiment of the invention, the CoA active site in its bound state comprises the relative structural coordinates according to Figure 2 and 2A-1 to 2A-19 of residues ARG45, PHE49, ARG53, LYS81, ASN84, GLY85, LYS86, PRO87, ILE103, THR104 and HIS105 from one monomer of ACPS, and of ASP8, GLU11, ARG14, MET18, PHE25, ARG28, ILE29, PHE54, GLU58, SER61, LYS62, GLY65, THR66, GLY67, ILE68 and PHE74 from a second monomer of ACPS, in each case ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å, or more preferably not more than 1.0Å, or most preferably, not more than 0.5Å.--

On page 17, lines 21-28:

--In an alternate embodiment, the active site comprises the relative structural coordinates according to Figure 2 and 2A-1 to 2A-19 of residues ARG53, ASN84, GLY85, LYS86, PRO87, ILE103, THR104, and HIS105 from one monomer of ACPS and of residues ASP8, PHE25, ARG28, ILE29, PHE54, GLU58, SER61, LYS62, GLY65, THR66, GLY67, ILE68 and PHE74 from a second monomer of ACPS, in each case ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å, or more preferably not more than 1.0Å, or most preferably, not more than 0.5Å.--

On page 18, lines 1-9:

--In a yet further embodiment, the active site comprises the relative structural coordinates according to Figure 2 and 2A-1 to 2A-19 of residues LEU41, ARG45, GLU48, PHE49, LEU50, ALA51, GLY52, ILE79, ARG80, LYS81, ASP82, GLN83, TYR88, VAL101, SER102, THR106, TYR109, ALA110, and ALA111 from one monomer of ACPS and of residues ILE5, GLY6, LEU7, ILE9, THR10, ARG14, ILE15, MET18, GLN22, ALA55, LYS57, ALA59, PHE60, ALA63, PHE64, GLY69, ARG70, GLN71 and LEU72 from a second monomer of ACPS, in each case ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å, or more preferably, not more than 1.0Å, and most preferably, not more than 0.5Å.--

On page 18, lines 10-14:

--Finally, a CoA active site of the present invention comprises the relative structural coordinates according to Figure 2 and 2A-1 to 2A-19 of GLY6, ASP8, ALA51, ARG53, LYS57, GLU58, ALA59, LYS62 and ALA63, ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å, or more preferably, not more than 1.0Å, and most preferably, not more than 0.5Å.--

On page 20, line 13 through page 21, line 6:

--The present invention is not limited to identifying agents which interact with an active site of ACPS or ACPS-CoA complex, but also is directed to a method for identifying an activator or inhibitor of any molecule or molecular complex comprising a CoA binding site, comprising the first step of generating a three dimensional model of said molecule or molecular complex comprising a CoA binding site using the relative structural coordinates according to Figure 1 and 1A-1 to 1A-107 or Figure 2 and 2A-1 to 2A-19 of residues ARG45, PHE49, ARG53, LYS81, ASN84, GLY85, LYS86, PRO87, ILE103, THR104 and HIS105 from one monomer of ACPS, and of ASP8, GLU11, ARG14, MET18, PHE25, ARG28, ILE29, PHE54, GLU58, SER61, LYS62, GLY65, THR66, GLY67, ILE68 and PHE74 from a second monomer of ACPS, in each case ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å, or more

preferably not more than 1.0Å, or most preferably, not more than 0.5Å. In alternate embodiments, the relative structural coordinates according to Figure 1 and 1A-1 to 1A-107 are from ACPS1 and ACPS2, respectively; from ACPS2 and ACPS3, respectively; from ACPS1 and ACPS3, respectively; from ACPS4 and ACPS5, respectively; from ACPS5 and ACPS6, respectively; and from ACPS4 and ACPS6, respectively. Then, a candidate activator or inhibitor is selected or designed by performing computer fitting analyses of said candidate agent with the three dimensional model of the molecule or molecular complex comprising a CoA active site. Once the candidate activator or inhibitor is obtained, it may be contacted with the molecule or molecular complex in order to measure the effect the candidate activator or inhibitor has on said molecule or molecular complex.--

On page 21, lines 7-24:

--Alternatively, the three dimensional structure of the molecule or molecular complex comprising a CoA binding site may be determined using (a) the relative structural coordinates according to Figure 1 and 1A-1 to 1A-107 or Figure 2 and 2A-1 to 2A-19 of residues ARG53, ASN84, GLY85, LYS86, PRO87, ILE103, THR104, and HIS105 from one monomer of ACPS and of residues ASP8, PHE25, ARG28, ILE29, PHE54, GLU58, SER61, LYS62, GLY65, THR66, GLY67, ILE68 and PHE74 from a second monomer of ACPS, or (b) of LEU41, ARG45, GLU48, PHE49, LEU50, ALA51, GLY52, ILE79, ARG80, LYS81, ASP82, GLN83, TYR88, VAL101, SER102, THR106, TYR109, ALA110, and ALA111 from one monomer of ACPS and of residues ILE5, GLY6, LEU7, ILE9, THR10, ARG14, ILE15, MET18, GLN22, ALA55, LYS57, ALA59, PHE60, ALA63, PHE64, GLY69, ARG70, GLN71 and LEU72 from a second monomer of ACPS, in each case ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å, or more preferably not more than 1.0Å, or most preferably, not more than 0.5Å. Again, in alternate embodiments, the relative structural coordinates according to Figure 1 and 1A-1 to 1A-107 are from ACPS1 and ACPS2, respectively; from ACPS2 and ACPS3, respectively; from ACPS1 and ACPS3, respectively; from ACPS4

and ACPS5, respectively; from ACPS5 and ACPS6, respectively; and from ACPS4 and ACPS6, respectively.---

Marked-up Pending Claims

Additions are underlined; deletions are indicated in square brackets.

15. (Amended) A method for identifying an agent that interacts with an active site of acyl carrier protein synthase (ACPS), comprising the steps of:

(a) obtaining a crystallized ACPS, wherein the crystallized ACPS is characterized as being in plate form with space group $P2_1$, and having unit cell parameters of a=76.26Å, b=76.16Å, c=85.69 Å, and beta=93.3°;

(b) obtaining the relative structural coordinates of the crystallized ACPS of step (a), wherein the relative structural coordinates are set forth in Figure 1 and 1A-1 to 1A-107;

(c) generating a three dimensional model of ACPS using the relative structural coordinates of the amino acids of ACPS obtained in step (b), ± a root mean square deviation from the backbone atoms of not more than 1.5Å;

[(a)] (d) determining an active site of ACPS from [a] said three dimensional model [of the ACPS enzyme]; and

[(b)] (e) performing computer fitting analysis to identify an agent which interacts with said active site.

16. The method of Claim 15, further comprising contacting the identified agent with ACPS in order to determine the effect the agent has on ACPS activity.

17. The method of Claim 16, wherein the agent is an inhibitor of ACPS activity.

18. (Withdrawn from Consideration by Examiner) The method of Claim 16, wherein the agent is an activator of ACPS activity.

19. (Amended) A method for identifying an agent that interacts with an active site of an acyl carrier protein synthase-coenzyme A (ACPS-CoA) complex, comprising the steps of:

(a) obtaining a crystallized complex comprising acyl carrier protein synthase (ACPS) and coenzyme A (CoA), wherein the crystallized complex is characterized as being in pyramidal form with space group R3, and having unit cell parameters of a=b=55.82Å and c=92.28Å;

(b) obtaining the relative structural coordinates of the amino acids of the crystallized complex of step (a), wherein the relative structural coordinates are set forth in Figure 2 and 2A-1 to 2A-19;

(c) generating a three dimensional model of ACPS-CoA using the relative structural coordinates of the amino acids obtained in step (b), ± a root mean square deviation from the backbone atoms of not more than 1.5Å;

[(a)] (d) determining an active site of the ACPS-CoA complex from [a] said three dimensional model [of the ACPS-CoA complex]; and

[(b)] (e) performing computer fitting analysis to identify an agent which interacts with said active site.

20. The method of Claim 19, further comprising contacting the identified agent with ACPS-CoA complex in order to determine the effect the agent has on ACPS-CoA complex activity.

21. The method of Claim 20, wherein the agent is an inhibitor of ACPS-CoA complex activity.

22. (Withdrawn from Consideration by Examiner) The method of Claim 21, wherein the agent is an activator of ACPS-CoA complex activity.

35. (New) A method for identifying an agent that interacts with an active site of acyl carrier protein synthase (ACPS), comprising the steps of:

(a) obtaining a crystallized complex comprising acyl carrier protein synthase (ACPS) and coenzyme A (CoA), wherein the crystallized complex is characterized as

being in pyramidal form with space group R3, and having unit cell parameters of a=b=55.82Å and c=92.28Å;

(b) obtaining the relative structural coordinates of the amino acids of the crystallized complex of step (a), wherein the relative structural coordinates are set forth in Figure 2 and 2A-1 to 2A-19;

(c) generating a three dimensional model of ACPS using the relative structural coordinates of the amino acids obtained in step (b), ± a root mean square deviation from the backbone atoms of not more than 1.5Å;

(d) determining an active site of ACPS from said three dimensional model; and

(e) performing computer fitting analysis to identify an agent which interacts with said active site.

36. (New) The method of Claim 35, further comprising contacting the identified agent with ACPS in order to determine the effect the agent has on ACPS activity.

37. (New) The method of Claim 36, wherein the agent is an inhibitor of ACPS activity.

38. (New) The method of claim 15, wherein the active site of ACPS determined in step (d) comprises the structural coordinates according to Figure 1 and 1A-1 to 1A-107 of amino acid residues ARG45, PHE49, ARG53, LYS81, ASN84, GLY85, LYS86, PRO87, ILE103, THR104 and HIS105 from one monomer of ACPS, and of ASP8, GLU11, ARG14, MET18, PHE25, ARG28, ILE29, PHE54, GLU58, SER61, LYS62, GLY65, THR66, GLY67, ILE68 and PHE74 from a second monomer of ACPS, ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å.

39. (New) The method of claim 15, wherein the active site of ACPS determined in step (d) comprises the structural coordinates according to Figure 1 and 1A-1 to 1A-107 of amino acid residues ARG53, ASN84, GLY85, LYS86, PRO87, ILE103, THR104,

and HIS105 from one monomer of ACPS and of amino acid residues ASP8, PHE25, ARG28, ILE29, PHE54, GLU58, SER61, LYS62, GLY65, THR66, GLY67, ILE68 and PHE74 from a second monomer of ACPS, ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å.

40. (New) The method of claim 15, wherein the active site of ACPS determined in step (d) comprises the structural coordinates according to Figure 1 and 1A-1 to 1A-107 of amino acid residues LEU41, ARG45, GLU48, PHE49, LEU50, ALA51, GLY52, ILE79, ARG80, LYS81, ASP82, GLN83, TYR88, VAL101, SER102, THR106, TYR109, ALA110, and ALA111 from one monomer of ACPS and of amino acid residues ILE5, GLY6, LEU7, ILE9, THR10, ARG14, ILE15, MET18, GLN22, ALA55, LYS57, ALA59, PHE60, ALA63, PHE64, GLY69, ARG70, GLN71 and LEU72 from a second monomer of ACPS, ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å.

41. (New) The method of claim 15, wherein the active site of ACPS determined in step (d) comprises the structural coordinates of amino acid residues GLY6, ASP8, ALA51, ARG53, LYS57, GLU58, ALA59, LYS62, and ALA63 according to Figure 1 and 1A-1 to 1A-107, ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å.

42. (New) The method of claim 35, wherein the active site of ACPS determined in step (d) comprises the structural coordinates according to Figure 2 and 2A-1 to 2A-19 of amino acid residues ARG45, PHE49, ARG53, LYS81, ASN84, GLY85, LYS86, PRO87, ILE103, THR104 and HIS105 from one monomer of ACPS, and of ASP8, GLU11, ARG14, MET18, PHE25, ARG28, ILE29, PHE54, GLU58, SER61, LYS62, GLY65, THR66, GLY67, ILE68 and PHE74 from a second monomer of ACPS, ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å.

43. (New) The method of claim 35, wherein the active site of ACPS determined in step (d) comprises the structural coordinates according to Figure 2 and 2A-1 to 2A-19 of amino acid residues ARG53, ASN84, GLY85, LYS86, PRO87, ILE103, THR104, and HIS105 from one monomer of ACPS and of amino acid residues ASP8, PHE25, ARG28, ILE29, PHE54, GLU58, SER61, LYS62, GLY65, THR66, GLY67, ILE68 and PHE74 from a second monomer of ACPS, ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å.

44. (New) The method of claim 35, wherein the active site of ACPS determined in step (d) comprises the structural coordinates according to Figure 2 and 2A-1 to 2A-19 of amino acid residues LEU41, ARG45, GLU48, PHE49, LEU50, ALA51, GLY52, ILE79, ARG80, LYS81, ASP82, GLN83, TYR88, VAL101, SER102, THR106, TYR109, ALA110, and ALA111 from one monomer of ACPS and of amino acid residues ILE5, GLY6, LEU7, ILE9, THR10, ARG14, ILE15, MET18, GLN22, ALA55, LYS57, ALA59, PHE60, ALA63, PHE64, GLY69, ARG70, GLN71 and LEU72 from a second monomer of ACPS, ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å.

45. (New) The method of claim 35, wherein the active site of ACPS determined in step (d) comprises the structural coordinates of amino acid residues GLY6, ASP8, ALA51, ARG53, LYS57, GLU58, ALA59, LYS62, and ALA63 according to Figure 2 and 2A-1 to 2A-19, ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å.

46. (New) The method of claim 15, wherein the ± root mean square deviation from the backbone atoms is not more than 1.0 Å.

47. (New) The method of claim 46, wherein the ± root mean square deviation from the backbone atoms is not more than 0.5 Å.

48. (New) The method of claim 19, wherein the ± root mean square deviation from the backbone atoms is not more than 1.0 Å.

49. (New) The method of claim 48, wherein the ± root mean square deviation from the backbone atoms is not more than 0.5 Å.

50. (New) The method of claim 35, wherein the ± root mean square deviation from the backbone atoms of said amino acids is not more than 1.0 Å.

51. (New) The method of claim 50, wherein the ± root mean square deviation from the backbone atoms of said amino acids is not more than 0.5 Å.

52. (New) The method of claim 38, wherein the ± root mean square deviation from the backbone atoms of said amino acids is not more than 1.0 Å.

53. (New) The method of claim 52, wherein the ± root mean square deviation from the backbone atoms of said amino acids is not more than 0.5 Å.

54. (New) The method of claim 39, wherein the ± root mean square deviation from the backbone atoms of said amino acids is not more than 1.0 Å.

55. (New) The method of claim 54, wherein the ± root mean square deviation from the backbone atoms of said amino acids is not more than 0.5 Å.

56. (New) The method of claim 40, wherein the ± root mean square deviation from the backbone atoms of said amino acids is not more than 1.0 Å.

57. (New) The method of claim 56, wherein the ± root mean square deviation from the backbone atoms of said amino acids is not more than 0.5 Å.

58. (New) The method of claim 41, wherein the ± root mean square deviation from the backbone atoms of said amino acids is not more than 1.0 Å.

59. (New) The method of claim 58, wherein the ± root mean square deviation from the backbone atoms of said amino acids is not more than 0.5 Å.

60. (New) The method of claim 42, wherein the ± root mean square deviation from the backbone atoms of said amino acids is not more than 1.0 Å.

61. (New) The method of claim 60, wherein the ± root mean square deviation from the backbone atoms of said amino acids is not more than 0.5 Å.

62. (New) The method of claim 43, wherein the ± root mean square deviation from the backbone atoms of said amino acids is not more than 1.0 Å.

63. (New) The method of claim 62, wherein the ± root mean square deviation from the backbone atoms of said amino acids is not more than 0.5 Å.

64. (New) The method of claim 44, wherein the ± root mean square deviation from the backbone atoms of said amino acids is not more than 1.0 Å.

65. (New) The method of claim 64, wherein the ± root mean square deviation from the backbone atoms of said amino acids is not more than 0.5 Å.

66. (New) The method of claim 45, wherein the ± root mean square deviation from the backbone atoms of said amino acids is not more than 1.0 Å.

67. (New) The method of claim 66, wherein the ± root mean square deviation from the backbone atoms of said amino acids is not more than 0.5 Å.

68. (New) A method for identifying an agent that interacts with an active site of acyl carrier protein synthase (ACPS), comprising the steps of:

(a) obtaining a crystallized ACPS, wherein the crystallized ACPS is characterized as being in plate form with space group $P2_1$, and having unit cell parameters of a=76.26Å, b=76.16Å, c=85.69 Å, and beta=93.3°;

(b) obtaining the relative structural coordinates of the crystallized ACPS of step (a);

(c) generating a three dimensional model of ACPS using the relative structural coordinates of the amino acids of ACPS obtained in step (b), ± a root mean square deviation from the backbone atoms of not more than 1.5Å;

(d) determining an active site of ACPS from said three dimensional model; and

(e) performing computer fitting analysis to identify an agent which interacts with said active site.

69. (New) The method of Claim 68, further comprising contacting the identified agent with ACPS in order to determine the effect the agent has on ACPS activity.

70. (New) The method of Claim 69, wherein the agent is an inhibitor of ACPS activity.

71. (New) A method for identifying an agent that interacts with an active site of an acyl carrier protein synthase-coenzyme A (ACPS-CoA) complex, comprising the steps of:

(a) obtaining a crystallized complex comprising acyl carrier protein synthase (ACPS) and coenzyme A (CoA), wherein the crystallized complex is characterized as being in pyramidal form with space group R3, and having unit cell parameters of a=b=55.82Å and c=92.28Å;

(b) obtaining the relative structural coordinates of the amino acids of the crystallized complex of step (a);

(c) generating a three dimensional model of ACPS-CoA using the relative structural coordinates of the amino acids obtained in step (b), ± a root mean square deviation from the backbone atoms of not more than 1.5Å;

(d) determining an active site of the ACPS-CoA complex from said three dimensional model; and

(e) performing computer fitting analysis to identify an agent which interacts with said active site.

72. (New) The method of Claim 71, further comprising contacting the identified agent with ACPS-CoA complex in order to determine the effect the agent has on ACPS-CoA complex activity.

73. (New) The method of Claim 72, wherein the agent is an inhibitor of ACPS-CoA complex activity.

74. (New) A method for identifying an agent that interacts with an active site of acyl carrier protein synthase (ACPS), comprising the steps of:

(a) obtaining a crystallized complex comprising acyl carrier protein synthase (ACPS) and coenzyme A (CoA), wherein the crystallized complex is characterized as being in pyramidal form with space group R3, and having unit cell parameters of a=b=55.82Å and c=92.28Å;

(b) obtaining the relative structural coordinates of the amino acids of the crystallized complex of step (a);

(c) generating a three dimensional model of ACPS using the relative structural coordinates of the amino acids obtained in step (b), ± a root mean square deviation from the backbone atoms of not more than 1.5Å;

(d) determining an active site of ACPS from said three dimensional model; and

(e) performing computer fitting analysis to identify an agent which interacts with said active site.

75. (New) The method of Claim 74, further comprising contacting the identified agent with ACPS in order to determine the effect the agent has on ACPS activity.

76. (New) The method of Claim 75, wherein the agent is an inhibitor of ACPS activity.

77. (New) The method of claim 68, wherein the active site of ACPS determined in step (d) comprises the structural coordinates of amino acid residues ARG45, PHE49, ARG53, LYS81, ASN84, GLY85, LYS86, PRO87, ILE103, THR104 and HIS105 from one monomer of ACPS, and of ASP8, GLU11, ARG14, MET18, PHE25, ARG28, ILE29, PHE54, GLU58, SER61, LYS62, GLY65, THR66, GLY67, ILE68 and PHE74 from a second monomer of ACPS, ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å.

78. (New) The method of claim 68, wherein the active site of ACPS determined in step (d) comprises the structural coordinates of amino acid residues ARG53, ASN84, GLY85, LYS86, PRO87, ILE103, THR104, and HIS105 from one monomer of ACPS and of amino acid residues ASP8, PHE25, ARG28, ILE29, PHE54, GLU58, SER61, LYS62, GLY65, THR66, GLY67, ILE68 and PHE74 from a second monomer of ACPS, ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å.

79. (New) The method of claim 68, wherein the active site of ACPS determined in step (d) comprises the structural coordinates of amino acid residues LEU41, ARG45, GLU48, PHE49, LEU50, ALA51, GLY52, ILE79, ARG80, LYS81, ASP82, GLN83, TYR88, VAL101, SER102, THR106, TYR109, ALA110, and ALA111 from one monomer of ACPS and of amino acid residues ILE5, GLY6, LEU7, ILE9, THR10, ARG14, ILE15, MET18, GLN22, ALA55, LYS57, ALA59, PHE60, ALA63, PHE64, GLY69, ARG70, GLN71 and

LEU72 from a second monomer of ACPS, ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å.

80. (New) The method of claim 68, wherein the active site of ACPS determined in step (d) comprises the structural coordinates of amino acid residues GLY6, ASP8, ALA51, ARG53, LYS57, GLU58, ALA59, LYS62, and ALA63, ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å.

81. (New) The method of claim 74, wherein the active site of ACPS determined in step (d) comprises the structural coordinates according of amino acid residues ARG45, PHE49, ARG53, LYS81, ASN84, GLY85, LYS86, PRO87, ILE103, THR104 and HIS105 from one monomer of ACPS, and of ASP8, GLU11, ARG14, MET18, PHE25, ARG28, ILE29, PHE54, GLU58, SER61, LYS62, GLY65, THR66, GLY67, ILE68 and PHE74 from a second monomer of ACPS, ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å.

82. (New) The method of claim 74, wherein the active site of ACPS determined in step (d) comprises the structural coordinates of amino acid residues ARG53, ASN84, GLY85, LYS86, PRO87, ILE103, THR104, and HIS105 from one monomer of ACPS and of amino acid residues ASP8, PHE25, ARG28, ILE29, PHE54, GLU58, SER61, LYS62, GLY65, THR66, GLY67, ILE68 and PHE74 from a second monomer of ACPS, ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å.

83. (New) The method of claim 74, wherein the active site of ACPS determined in step (d) comprises the structural coordinates of amino acid residues LEU41, ARG45, GLU48, PHE49, LEU50, ALA51, GLY52, ILE79, ARG80, LYS81, ASP82, GLN83, TYR88, VAL101, SER102, THR106, TYR109, ALA110, and ALA111 from one monomer of ACPS and of amino acid residues ILE5, GLY6, LEU7, ILE9, THR10, ARG14, ILE15, MET18, GLN22, ALA55, LYS57, ALA59, PHE60, ALA63, PHE64, GLY69, ARG70, GLN71 and

LEU72 from a second monomer of ACPS, ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å.

84. (New) The method of claim 74, wherein the active site of ACPS determined in step (d) comprises the structural coordinates of amino acid residues GLY6, ASP8, ALA51, ARG53, LYS57, GLU58, ALA59, LYS62, and ALA63, ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å.